SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: (US ONLY) S. COREY, J. ADAMS, C. PRINT, D.C.S.

 HUANG, L. O'CONNOR, A. STRASSER, H. PUTHALAKATH,
 L. O'REILLY

 (OTHER THAN US) THE WALTER AND ELIZA HALL
 INSTITUTE OF MEDICAL RESEARCH
 - (ii) TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES
 - (iii) NUMBER OF SEQUENCES: 26
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIES COLLISON CAVE
 - (B) STREET: 1 LITTLE COLLINS STREET
 - (C) CITY: MELBOURNE
 - (D) STATE: VICTORIA
 - (E) COUNTRY: AUSTRALIA
 - (F) ZIP: 3000
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT INTERNATIONAL
- (B) FILING DATE: 17 SEPTEMBER 1998

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PO9263
- (B) FILING DATE: 17 SEPTEMBER 1997

PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PO9373
- (B) FILING DATE: 24 SEPTEMBER 1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: HUGHES, DR E JOHN L
- (C) REFERENCE/DOCKET NUMBER: EJH/DK

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: +61 3 9254 2777
- (B) TELEFAX: +61 3 9254 2770
- (C) TELEX: AA 31787

110

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(2)	INFO	RMAT	CION	FOR	SEQ	ID 1	10:1:	:								
	(i)	(E	L) LE 3) TY C) ST	ENGTH PE: PRANI	HARAC H: 33 nucl DEDNE	3 nu .eic ESS:	acio sino	otide 1	es							
	(ii)	MOI	LECUI	E TY	PE:	DNA										
		(<i>F</i>	3) L(ME/F	CEY: ION: ESCRI	13		SEQ]	D NC):1:			·			
ATG	GCC	AAG	CAA	CCT	TCT	GAT	GTA	AGT	TCT	GAG	TGT	GAC	AGA	GAA	GGT	48
Met	Ala	Lys	Gln	Pro	Ser	Asp	Val	Ser	Ser	Glu	Cys	Asp	Arg	Glu	Gly	
1				5					10					15		
GGA	CAA	TTG	CAG	CCT	GCT	GAG	AGG	CCT	CCC	CAG	CTC	AGG	CCT	GGG	GCC	96
Gly	Gln	Leu	Gln	Pro	Ala	Glu	Arg	Pro	Pro	Gln	Leu	Arg	Pro	Gly	Ala	
			20					25					30			
CCT	ACC	TCC	CTA	CAG	ACA	GAA	CCG	CAA	GCT	TCC	ATA	CGA	CAG	TCT	CAG	144
Pro	Thr	Ser	Leu	Gln	Thr	Glu	Pro	Gln	Ala	Ser	Ile	Arg	Gln	Ser	Gln	
		35					40					45				
GAG	GAA	CCT	GAA	GAT	CTG	CGC	CCG	GAG	ATA	CGG	ATT	GCA	CAG	GAG	CTG	192
Glu	Glu	Pro	Glu	Asp	Leu	Arg	Pro	Glu	Ile	Arg	Ile	Ala	Gln	Glu	Leu	
	50					55					60					
CGG	CGG	ATC	GGA	GAC	GAG	TTC	AAC	GAA	ACT	TAC	ACA	AGG	AGG	GTG	TTT	240
Arg	Arg	Ile	Gly	Asp	Glu	Phe	Asn	Glu	Thr	Tyr	Thr	Arg	Arg	Val	Phe	
65					70					75					80	
GCA	AAT	GAT	TAC	CGC	GAG	GCT	GAA	GAC	CAC	CCT	CAA	ATG	GTT	ATC	TTA	288
Ala	Asn	Asp	Tyr	Arg	Glu	Ala	Glu	Asp	His	Pro	Gln	Met	Val	Ile	Leu	
				85					90					95		

CAA CTG TTA CGC TTT ATC TTC CGT CTG GTA TGG AGA AGG CAT TG

105

Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His

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- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly

1 5 10 15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala 20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln 35 40 45

Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
50 55 60

Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
65 70 75 80

Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu 85 90 95

Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
100 105 110

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 nucleotides
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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	(ii)	MOI	LECUI	LE TY	PE:	DNA										
	(ix)	(I	ATURE A) NA B) LO	ME/F			123									
	(xi)	SEÇ	QUENC	CE DE	ESCR	PTIC	ON: S	SEQ I	D NO	0:3:						
ATG	GCC	AAG	CAA	CCT	TCT	GAT	GTA	AGT	TCT	GAG	TGT	GAC	AGA	GAA	GGT	48
	Ala	Lys	Gln		Ser	Asp	Val	Ser		Glu	Cys	Asp	Arg		Gly	
1				5					10					15		
GGA	CAA	TTG	CAG	CCT	GCT	GAG	AGG	CCT	CCC	CAG	CTC	AGG	CCT	GGG	GCC	96
Gly	Gln	Leu	Gln	Pro	Ala	Glu	Arg	Pro	Pro	Gln	Leu	Arg	Pro	Gly	Ala	
			20					25					30			
CCT	ACC	TCC	CTA	CAG	ACA	GAA	CCG	CAA	GAC	AGG	AGC	CCG	GCA	CCC	ATG	144
			Leu													
		35					40					45				
AGT	TGT	GAC	AAG	TCA	ACA	CAA	ACC	CCA	AGT	CCT	CCT	TGC	CAG	GCC	TTC	192
			Lys													
	50					55					60					
AAC	CAC	TAT	CTC	AGT	GCA	ATG	GCT	TCC	ATA	CGA	CAG	TCT	CAG	GAG	GAA	240
Asn	His	Tyr	Leu	Ser	Ala	Met	Ala	Ser	Ile	Arg	Gln	Ser	Gln	Glu	Glu	
65					70					75					80	
CCT	GAA	GAT	CTG	CGC	CCG	GAG	ATA	CGG	ATT	GCA	CAG	GAG	CTG	CGG	CGG	288
Pro	Glu	Asp	Leu	Arg	Pro	Glu	Ile	Arg	Ile	Ala	Gln	Glu	Leu	Arg	Arg	
				85					90					95		
ATC	GGA	GAC	GAG	TTC	AAC	GAA	ACT	TAC	ACA	AGG	AGG	GTG	TTT	GCA	AAT	336
Ile	Gly	Asp	Glu	Phe	Asn	Glu	Thr	Tyr	Thr	Arg	Arg	Val	Phe	Ala	Asn	
			100					105					110			
GAT	TAC	CGC	GAG	GCT	GAA	GAC	CAC	CCT	CAA	ATG	GTT	ATC	TTA	CAA	CTG	384
Asp	Tyr	Arg	Glu	Ala	Glu	Asp	His	Pro	Gln	Met	Val	Ile	Leu	Gln	Leu	
		115					120					125				

TTA CGC TTT ATC TTC CGT CTG GTA TGG AGA AGG CAT TG
Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
130 135 140

423

(2) INFORMATION FOR SEQ ID NO:4:

(1)

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly

1 10 15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala 20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met 35 40 45

Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe 50 55 60

Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu 65 70 75 80

Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg 85 90 95

Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn 100 105 110

Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu 115 120 125

Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
130 135 140

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(2)	INFORMATION	FOR	SEO	ID	NO:5:
	T *** O * ** T T T O T !	1 010	-		110.0.

(i)	CECTIENCE	CHARACTERISTICS	
111	SECUENCE	CHARACTERISTICS	•

(A) LENGTH: 591 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	GCC	AAG	CAA	CCT	TCT	GAT	GTA	AGT	TCT	GAG	TGT	GAC	AGA	GAA	GGT	48
Met	Ala	Lys	Gln	Pro	Ser	Asp	Val	Ser	Ser	Glu	Cys	Asp	Arg	Glu	Gly	
1				5					10					15		
GGA	CAA	TTG	CAG	CCT	GCT	GAG	AGG	CCT	CCC	CAG	CTC	AGG	CCT	GGG	GCC	96
Gly	Gln	Leu	Gln	Pro	Ala	Glu	Arg	Pro	Pro	Gln	Leu	Arg	Pro	Gly	Ala	
			20					25					30			
CCT	ACC	TCC	CTA	CAG	ACA	GAA	CCG	CAA	GGT	TAA	CCC	GAC	GGC	GAA	GGG	144
Pro	Thr	Ser	Leu	Gln	Thr	Glu	Pro	Gln	Gly	Asn	Pro	Asp	Gly	Glu	Gly	
		35					40					45				
GAC	CGC	TGC	CCC	CAC	GGC	AGC	CCT	CAG	GGC	CCG	CTG	GCC	CCA	CCG	GCC	192
Asp	Arg	Cys	Pro	His	${\tt Gly}$	Ser	Pro	Gln	Gly	Pro	Leu	Ala	Pro	Pro	Ala	
	50					55					60					
AGC	CCT	GGC	CCT	TTT	GCT	ACC	AGA	TCC	CCA	CTT	TTC	ATC	TTT	GTG	AGA	240
Ser	Pro	Gly	Pro	Phe	Ala	Thr	Arg	Ser	Pro	Leu	Phe	Ile	Phe	Val	Arg	
65					70					75					80	
AGA	TCT	TCT	CTG	CTG	TCC	CGG	TCC	TCC	AGT	GGG	TAT	TTC	TCT	TTT	GAC	288
Arg	Ser	Ser	Leu	Leu	Ser	Arg	Ser	Ser	Ser	Gly	Tyr	Phe	Ser	Phe	Asp	
				85					90					95		

ACA GAC AGG AGC CCG GCA CCC ATG AGT TGT GAC AAG TCA ACA CAA ACC

Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr

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	100			105			110			
AGT Ser										384
ATA Ile 130									,	432
ATT Ile										480
ACA Thr										528
CAA Gln						_				57€
AGA Arq		TG								591

(2) INFORMATION FOR SEQ ID NO:6:

195

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met 1	Ala	Lys	Gln	Pro 5	Ser	Asp	Val	Ser	Ser 10	Glu	Cys	Asp	Arg	Glu 15	Gly
Gly	Gln	Leu	Gln 20	Pro	Ala	Glu	Arg	Pro 25	Pro	Gln	Leu	Arg	Pro 30	Gly	Ala
Pro	Thr	Ser 35	Leu	Gln	Thr	Glu	Pro 40	Gln	Gly	Asn	Pro	Asp 45	Gly	Glu	Gly
Asp	Arg 50	Cys	Pro	His	Gly	Ser 55	Pro	Gln	Gly	Pro	Leu 60	Ala	Pro	Pro	Ala
Ser 65	Pro	Gly	Pro	Phe	Ala 70	Thr	Arg	Ser	Pro	Leu 75	Phe	Ile	Phe	Val	Arc 80
Arg	Ser	Ser	Leu	Leu 85	Ser	Arg	Ser	Ser	Ser 90	Gly	Tyr	Phe	Ser	Phe 95	Asp
Thr	Asp	Arg	Ser 100	Pro	·Ala	Pro	Met	Ser 105	Cys	Asp	Lys	Ser	Thr 110	Gln	Thr
Pro	Ser	Pro 115	Pro	Cys	Gln	Ala	Phe 120	Asn	His	Tyr	Leu	Ser 125	Ala	Met	Ala
Ser	Ile 130	Arg	Gln	Ser	Gln	Glu 135	Glu	Pro	Glu	Asp	Leu 140	Arg	Pro	Glu	Ile
Arg 145	Ile	Ala	Gln	Glu	Leu 150	Arg	Arg	Ile	Gly	Asp 155	Glu	Phe	Asn	Glu	Th:
Tyr	Thr	Arg	Arg	Val 165	Phe	Ala	Asn	Asp	Tyr 170	Arg	Glu	Ala	Glu	Asp 175	His
Pro	Gln	Met	Val 180	Ile	Leu	Gln	Leu	Leu 185	Arg	Phe	Ile	Phe	Arg 190	Leu	Va]

Trp Arg Arg His

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(2)	INFO	RMAT	TION	FOR	SEQ	ID N	10:7:	:								
	(i)	(<i>E</i> (C	A) LE 3) TY C) ST	ENGTH PE: PRANI	H: 41 nucl	CTERI 17 nu 1eic ESS: line	acio sing	otide 1	es							
	(ii)	MOI	LECUI	E TY	PE:	DNA										
		(E	A) NA B) LO	ME/I		14		SEQ I	D NO):7:						
ATG	GCA	AAG	CAA	CCT	TCT	GAT	GTA	AGT	TCT	GAG	TGT	GAC	CGA	GAA	GGT	48
	Ala	Lys	Gln		Ser	Asp	Val	Ser		Glu	Cys	Asp	Arg		Gly	
1				5					10					15		
AGA	CAA	TTG	CAG	CCT	GCG	GAG	AGG	CCT	CCC	CAG	CTC	AGA	CCT	GGG	GCC	96
Arg	Gln	Leu	Gln 20	Pro	Ala	Glu	Arg	Pro 25	Pro	Gln	Leu	Arg	Pro 30	Gly	Ala	
CCT	ACC	TCC	CTA	CAG	ACA	GAG	CCA	CAA	GAC	AGG	AGC	CCA	GCA	CCC	ATG	144
Pro	Thr	Ser 35	Leu	Gln	Thr	Glu	Pro 40	Gln	Asp	Arg	Ser	Pro 45	Ala	Pro	Met	
AGT	TGT	GAC	AAA	TCA	ACA	CAA	ACC	CCA	AGT	CCT	CCT	TGC	CAG	GCC	TTC	192
Ser	Суs 50	qaA	Lys	Ser	Thr	Gln 55	Thr	Pro	Ser	Pro	Pro 60	Cys	Gln	Ala	Phe	
AAC	CAC	TAT	CTC	AGT	GCA	ATG	GCT	TCC	ATG	AGG	CAG	GCT	GAA	CCT	GCA	240
Asn	His	Tyr	Leu	Ser	Ala	Met	Ala	Ser	Met	Arg	Gln	Ala	Glu	Pro	Ala	
65					70					75					80	
GAT	ATG	CGC	CCA	GAG	ATA	TGG	ATC	GCC	CAA	GAG	TTG	CGG	CGT	ATC	GGA	288
Asp	Met	Arg	Pro	Glu	Ile	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	
				85					90					95		

GAC GAG TTT AAC GCT TAC TAT GCA AGG AGG GTA TTT TTG AAT AAT TAC 336
Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
100 105 110

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			GAA Glu													384
		115					120					125				
			CGC							TG						417
Tyr	Ile	Val	Arg	Leu	Val	Trp	Arg	Met	His							
	130					135										
(2)	INFO	ORMAT	NOIT	FOR	SEQ	ID N	10 : 8 :	:								
	((i) S	SEQUE	ENCE	CHAI	RACTE	ERIST	rics:	:							
			(A)	LEN	IGTH:	138	3 ami	ino a	acids	3						
						amino										
			(D)	TOE	OLOC	3Y:]	linea	ar								
		. .				_		_								
	()	L1) N	MOLEC	ULE	TYPE	E: pı	rote	ın								
	(>	ci) S	SEQUE	ENCE	DES	CRIPT	rion:	: SE(Q ID	NO:8	3:					
Met	Ala	Lys	Gln	Pro	Ser	Asp	Val	Ser	Ser	Glu	Cys	Asp	Arg	Glu	Gly	
1				5					10					15		
Arg	Gln	Leu	Gln	Pro	Ala	Glu	Arg	Pro	Pro	Gln	Leu	Arg	Pro	Gly	Ala	
			20					25					30			
Pro	Thr	Ser	Leu	Gln	Thr	Glu	Pro	Gln	Asp	Arg	Ser	Pro	Ala	Pro	Met	
		35					40					45				
_	_			_												
Ser		Asp	Lys	Ser	Thr		Thr	Pro	Ser	Pro		Cys	Gln	Ala	Phe	
	50					55					60					
λαν	uic	Ту гу г	T 011	Cor	ת ה ה	Mot	7.1 a	Cox	Mot	7 ~~~	C1 ~	77-	G1	Dane	77.0	
65	птъ	IYI	Leu	261	70	Mec	AIA	Ser	Met		GTII	Ald	Gru	PIO		
03					70					75					80	
Asp	Met.	Ara	Pro	Glu	Tle	Tro.	Tle	Δla	Gln	Glu	Len	Δνα	Ara	Tle	Glv	
		5		85					90	014	Dea	****9	****9	95	Cry	
Asp	Glu	Phe	Asn	Ala	Tyr	Tyr	Ala	Arg	Arg	Val	Phe	Leu	Asn	Asn	Tyr	
-			100		-	-		105					110		-	
Gln	Ala	Ala	Glu	Asp	His	Pro	Arg	Met	Val	Ile	Leu	Arg	Leu	Leu	Arg	

120

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Tyr Ile Val Arg Leu Val Trp Arg Met His 130 135 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 597 nucleotides (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: The last feet me (A) NAME/KEY: CDS (B) LOCATION: 1..597 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: M ATG GCA AAG CAA CCT TCT GAT GTA AGT TCT GAG TGT GAC CGA GAA GGT 48 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly ja k 1 5 10 15 AGA CAA TTG CAG CCT GCG GAG AGG CCT CCC CAG CTC AGA CCT GGG GCC 96 Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala 20 25 CCT ACC TCC CTA CAG ACA GAG CCA CAA GGT AAT CCT GAA GGC AAT CAC 144 Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His 35 40

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Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
65 70 75 80

ATC TTT ATG AGA AGA TCC TCC CTG CTG TCT CGA TCC TCC AGT GGG TAT 288

Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr

90

192

240

95

GGA GGT GAA GGG GAC AGC TGC CCC CAC GGC AGC CCT CAG GGC CCG CTG

Gly Glu Glu Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu

GCC CCA CCT GCC AGC CCT GGC CCT TTT GCT ACC AGA TCC CCG CTT TTC

55

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TTC	TCT	TTT	GAC	ACA	GAC	AGG	AGC	CCA	GCA	CCC	ATG	AGT	TGT	GAC	AAA	336
Phe	Ser	Phe	Asp	Thr	qaA	Arg	Ser	Pro	Ala	Pro	Met	Ser	Cys	Asp	Lys	
			100					105					110			
TCA	ACA	CAA	ACC	CCA	AGT	CCT	CCT	TGC	CAG	GCC	TTC	AAC	CAC	TAT	CTC	384
Ser	Thr	Gln	Thr	Pro	Ser	Pro	Pro	Cys	Gln	Ala	Phe	Asn	His	Tyr	Leu	
		115					120	_				125				
AGT	GCA	ATG	GCT	TCC	ATG	AGG	CAG	GCT	GAA	CCT	GCA	GAT	ATG	CGC	CCA	432
Ser	Ala	Met	Ala	Ser	Met	Arg	Gln	Ala	Glu	Pro	Ala	Asp	Met	Arg	Pro	
	130					135					140					
GAG	ATA	TGG	ATC	GCC	CAA	GAG	TTG	CĢG	CGT	ATC	GGA	GAC	GAG	TTT	AAC	480
Glu	Ile	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Asn	
145					150					155					160	
GCT	TAC	TAT	GCA	AGG	AGG	GTA	TTT	\mathtt{TTG}	AAT	AAT	TAC	CAA	GCA	GCC	GAA	528
Ala	Tyr	Tyr	Ala	Arg	Arg	Val	Phe	Leu	Asn	Asn	Tyr	Gln	Ala	Ala	Glu	
				165					170					175		
GAC	CAC	CCA	CGA	ATG	GTT	ATC	TTA	CGA	CTG	TTA	CGT	TAC	ATT	GTC	CGC	576
Asp	His	Pro	Arg	Met	Val	Ile	Leu	Arg	Leu	Leu	Arg	Tyr	Ile	Val	Arg	
			180					185					190			
CTG	GTG	TGG	AGA	ATG	CAT	TG										597
Leu	Val	Trp	Arg	Met	His											
		195														

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

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Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala 20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
35 40 45

Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
50 55 60

Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe 65 70 75 80

Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
85 90 95

Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
100 105 110

Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu 115 120 125

Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro 130 135 140

Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn 145 150 155 160

Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu 165 170 175

Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg 180 185 190

Leu Val Trp Arg Met His 195

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Tyr Lys Asp Asp Asp Lys

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Tyr Met Pro Met Glu 5

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- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Arg Arg Ile Gly Asp Glu
1 5

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGGGAGAACA GGGTACATCG ATGCGGG

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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GTGAACTGGG AGCGGATTGT GG	22
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 nucleotides(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CACCTGCACA CCGCGATCCA GGATAACG	28
(2) INFORMATION FOR SEQ ID NO:17:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 nucleotides (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
AGGATCCACC ATGGCCAAGC AACC	24
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 nucleotides(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRI	PTION: SEQ ID NO:18:	
GTTCTAGATC AGCACATCTC TC	rgggatag aaccac	36
(2) INFORMATION FOR SEQ	ID NO:19:	
(i) SEQUENCE CHARACT (A) LENGTH: 27 (B) TYPE: nucle (C) STRANDEDNE: (D) TOPOLOGY:	nucleotides eic acid SS: single	
(ii) MOLECULE TYPE:	DNA	
(xi) SEQUENCE DESCRI	PTION: SEQ ID NO:19:	
GCAAGCTTCCT GTGCAATCCG T.	ATCTCC	27
(2) INFORMATION FOR SEQ (i) SEQUENCE CHARAC (A) LENGTH: 30	TERISTICS:	
(B) TYPE: nucl		
(C) STRANDEDNE (D) TOPOLOGY:	_	
(ii) MOLECULE TYPE:	DNA	
(xi) SEQUENCE DESCRI	PTION: SEQ ID NO:20:	
GGAAGCTTGC AACGAAACTT AC	ACAAGGTG	30
(2) INFORMATION FOR SEQ	ID NO:21:	
(i) SEQUENCE CHARAC		
(A) LENGTH: 24 (B) TYPE: nucl		
(C) STRANDEDNE		

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GCAAGCTTCC GGGCGCAGAT CTTC	24
(2) INFORMATION FOR SEQ ID NO:22:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 28 nucleotides	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
CAAAGCTTCC TGTGCAATCC GTATCTCC	28
(2) INFORMATION FOR SEQ ID NO:23:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 30 nucleotides	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
GGAAGCTTTG AACGAAACTT ACACAAGGTG	30
(2) INFORMATION FOR SEO ID NO:24:	

- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CAAAGCTTCC GGGCGCAGAT CTTC	23
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 nucleotides(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
TAAGTTCTGA GTGTGACAGA GAAGGTGG	28
(2) INFORMATION FOR SEQ ID NO:26:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGTTGTAAG ATAACCATTT GAGGGTGG